

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

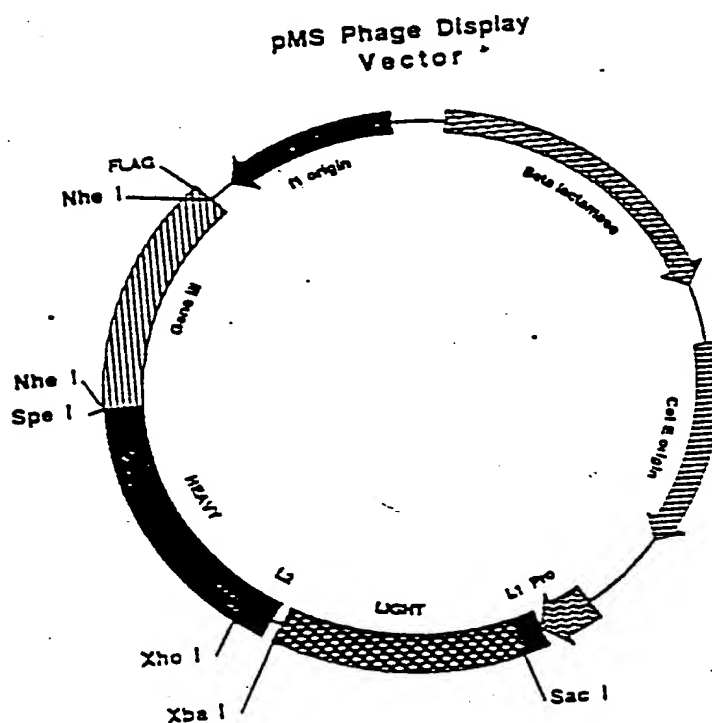
- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

FIGURE 1

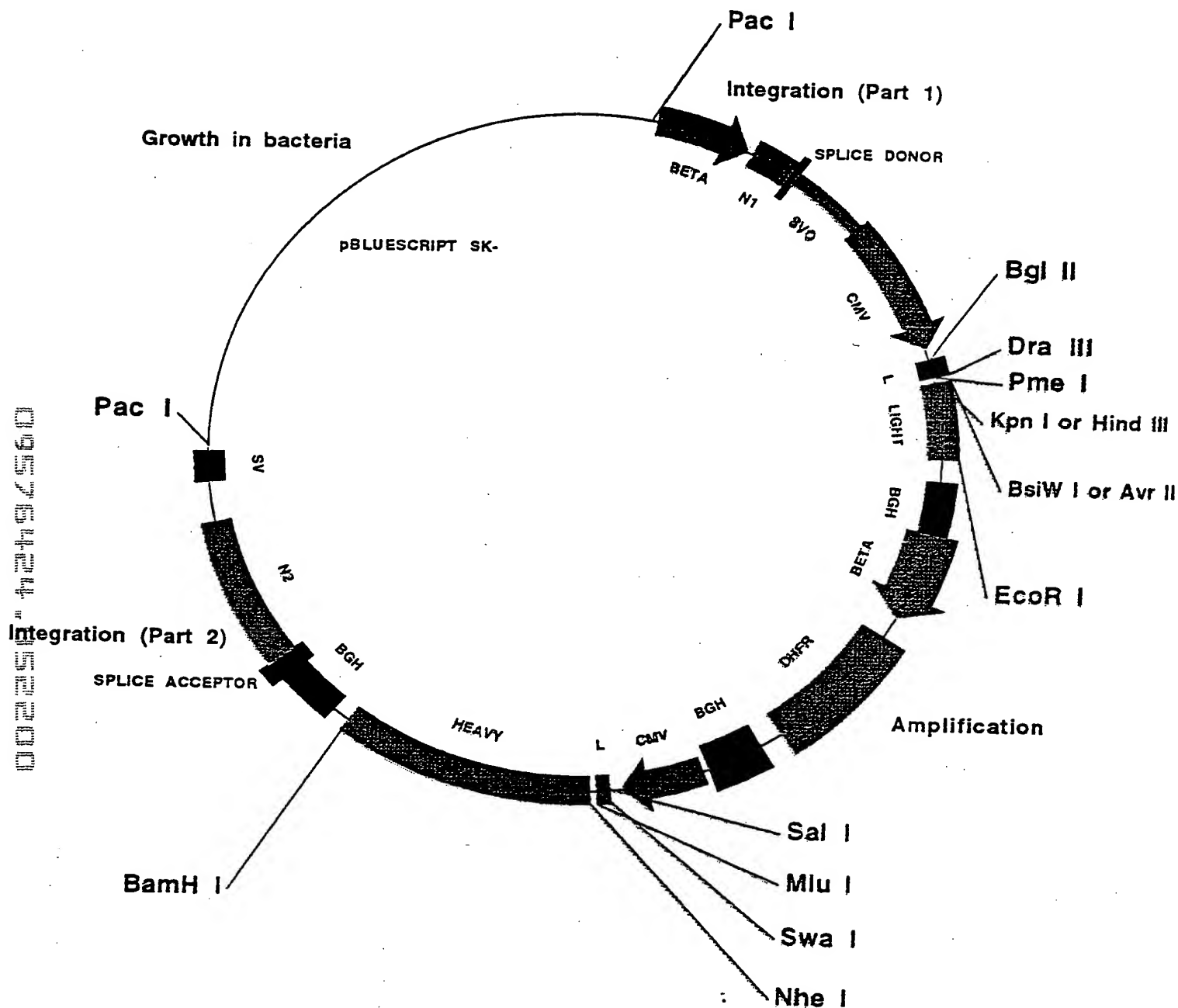
Figure 1: pMS Phage Display Vector. Pro = Lac Z promoter. L1 = Omp A leader. L2 = Pel B leader. Light = light chain. Heavy = heavy chain.



002250.42492560

FIGURE 2

NEOSPLA



- CMV = Cytomegalovirus promoter/enhancer
- BETA = Mouse Beta globin major promoter
- SVO = SV40 origin
- BGH = Bovine growth hormone polyadenylation
- SV = SV40 polyadenylation
- N1 = Neomycin phosphotransferase exon 1
- N2 = Neomycin phosphotransferase exon 2
- LIGHT = Human immunoglobulin kappa or lambda constant region
- DHFR = Dihydrofolate Reductase
- HEAVY = Human immunoglobulin gamma 1 or gamma 4 PE constant region
- L = Leader

Frame 1	M	R	V	P	A	Q	L	L	G	L	L	L	L	W	L	P	G	A	R	
	ATG	AGG	GTC	CCC	GCT	CAG	CTC	CTG	GGG	CTC	CTG	CTG	CTC	TGG	CTC	CCA	GGT	GCA	CGA	
			9			18			27			36			45			54		
C	A	Y	E	L	T	Q	P	P	S	V	S	V	S	P	G	Q	T	A	R	I
TGT	GCC	TAT	GAA	CTG	ACT	CAG	CCA	CCC	TCG	GTG	TCA	GTG	TCC	CCA	GGA	CAG	ACG	GCC	AGG	ATC
	63			72			81			90			99			108			117	
T	C	G	G	D	N	S	R	N	E	Y	V	H	W	Y	Q	Q	K	P	A	R
ACC	TGT	GGG	GGA	GAC	AAC	AGT	AGA	AAT	GAA	TAT	GTC	CAC	TGG	TAC	CAG	CAG	AAG	CCA	GCG	CGG
	126			135			144			153			162			171			180	
A	P	I	L	V	I	Y	D	D	S	D	R	P	S	G	I	P	E	R	F	S
GCC	CCT	ATA	CTG	GTC	ATC	TAT	GAT	GAT	AGT	GAC	CGG	CCC	TCA	GGG	ATC	CCT	GAG	CGA	TTC	TCT
	189			198			207			216			225			234			243	
G	S	K	S	G	N	T	A	T	L	T	I	N	G	V	E	A	G	D	E	A
GCC	TCC	AAA	TCA	GGG	AAC	ACC	GCC	ACC	CTG	ACC	ATC	AAC	GGG	GTC	GAG	GCC	GGG	GAT	GAG	GCT
	252			261			270			279			288			297			306	
D	Y	Y	C	Q	V	W	D	R	A	S	D	H	P	V	F	G	G	G	T	R
GAC	TAT	TAC	TGT	CAG	GTG	TGG	GAC	AGG	GCT	AGT	GAT	CAT	CCG	GTC	TTC	GGA	GGA	GGG	ACC	CGG
	315			324			333			342			351			360			369	
V	T	V	L	G	Q	P	K	A	A	P	S	V	T	L	F	P	P	S	S	E
GTG	ACC	GTC	CTA	GGT	CAG	CCC	AAG	GCT	GCC	CCC	TCG	GTC	ACT	CTG	TTC	CCG	CCC	TCC	TCT	GAG
	378			387			396			405			414			423			432	
E	L	Q	A	N	K	A	T	L	V	C	L	I	S	D	F	Y	P	G	A	V
GAG	CTT	CAA	GCC	AAC	AAG	GCC	ACA	CTG	GTG	TGT	CTC	ATA	AGT	GAC	TTC	TAC	CCG	GGA	GCC	GTG
	441			450			459			468			477			486			495	
T	V	A	W	K	A	D	S	S	P	V	K	A	G	V	E	T	T	T	P	S
ACA	GTG	GCC	TGG	AAG	GCA	GAT	AGC	AGC	CCC	GTC	AAG	GCG	GGA	GTG	GAG	ACC	ACC	ACA	CCC	TCC
	504			513			522			531			540			549			558	
K	Q	S	N	N	K	Y	A	A	S	S	Y	L	S	L	T	P	E	Q	W	K
AAA	CAA	AGC	AAC	AAC	AAG	TAC	GCG	GCC	AGC	AGC	TAC	CTG	AGC	CTG	ACG	CCT	GAG	CAG	TGG	AAG
	567			576			585			594			603			612			621	
S	H	R	S	Y	S	C	Q	V	T	H	E	G	S	T	V	E	K	T	V	A
TCC	CAC	AGA	AGC	TAC	AGC	TGC	CAG	GTC	ACG	CAT	GAA	GGG	AGC	ACC	GTG	GAG	AAG	ACA	GTG	GCC
	630			639			648			657			666			675			684	
P	T	E	C	S	.			</												

FIGURE 3b

Length of 7C10 heavy/Primatized: 1431 bp; Listed from: 1 to: 1431;
Translated from: 1 to: 1429 (Entire region);
Genetic Code used: Universal; Fri, May 26, 1995 11:11 AM

Frame 1 M K H L W F F L L L V A A P R W V L S
ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA A GCT CCC AGA TGG GTC CTG TCC
9 18 27 36 45 54
Q V K L Q Q W G E G L L Q P S E T L S R T
CAG GTG AAG CTG CAG CAG TGG GGC GAA GGA CTT CTG CAG CCT TCG GAG ACC CTG TCC CGC ACC
63 72 81 90 99 108 117
C V V S G G S I S G Y Y Y W T W I R Q T P
TGC GTT GTC TCT GGT GGC TCC ATC AGC GGT TAC TAC TAC TGG ACC TGG ATC CGC CAG ACC CCA
126 135 144 153 162 171 180
G R G L E W I G H I Y G N G A T T N Y N P
GGG AGG GGA CTG GAG TGG ATT GGC CAT ATT TAT GGT AAT GGT GCG ACC ACC AAC TAC AAT CCC
189 198 207 216 225 234 243
L K S R V T I S K D T S K N Q F F L N L
TCC CTC AAG AGT CGA GTC ACC ATT TCA AAA GAC ACG TCC AAG AAC CAG TTC TTC CTG AAC TTG
252 261 270 279 288 297 306
S V T D A D T A V Y Y C A R G P R P D C
AAT TCT GTG ACC GAC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGA GGC CCT CGC CCT GAT TGC
315 324 333 342 351 360 369
T I C Y G G W V D V W G P G D L V T V S
ACA ACC ATT TGT TAT GGC GGC TGG GTC GAT GTC TGG GGC CCG GGA GAC CTG GTC ACC GTC TCC
378 387 396 405 414 423 432
A S T K G P S V F P L A P S S K S T S G
TCA GCT AGC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG
441 450 459 468 477 486 495
G T A A L G C L V K D Y F P E P V T V S W
GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG
504 513 522 531 540 549 558
N S G A L T S G V H T F P A V L Q S S G L
AAC TCA GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC
567 576 585 594 603 612 621
Y S L S S V V T V P S S S L G T Q T Y I C
TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC TAC ATC TGC
630 639 648 657 666 675 684
N V N H K P S N T K V D K K A E P K S C D
AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GCA GAG CCC AAA TCT TGT GAC
693 702 711 720 729 738 747
K T H T C P P C P A P E L L G G P S V F L
AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC
756 765 774 783 792 801 810
F P P K P K D T L M I S R T P E V T C V V
TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG
819 828 837 846 855 864 873
V D V S H E D P E V K F N W Y V D G V E V
GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG
882 891 900 909 918 927 936

FIGURE 3b (Continued)

H	N	A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S	V
CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC
945				954			963			972			981			990			999	
L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K	V	S	N	K
CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	TCC	AAC	AAA
1008			1017			1026			1035		1044		1053					1062		
A	L	P	A	P	I	E	K	T	I	S	K	A	K	G	Q	P	R	E	P	Q
GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAA	CCA	CAG
1071			1080			1089			1098		1107		1116					1125		
V	Y	T	L	P	P	S	R	D	E	L	T	K	N	Q	V	S	L	T	C	L
GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG
1134			1143			1152			1161		1170		1179					1188		
V	K	G	F	Y	P	S	D	I	A	V	E	W	E	S	N	G	Q	P	E	N
GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC
1197			1206			1215			1224		1233		1242					1251		
N	Y	K	T	T	P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K	L
AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC
1260			1269			1278			1287		1296		1305					1314		
T	V	D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	H	E	A
ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT
1323			1332			1341			1350		1359		1368					1377		
L	H	N	H	Y	T	Q	K	S	L	S	L	S	P	G	K	.				
CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA				
1386			1395			1404			1413		1422		1431							

002250-24-152200

FIGURE 4a

Length of 7B6 light/Primatized: 720 bp; Listed from: 1 to: 720;
Translated from: 1 to: 718 (Entire region);
Genetic Code used: Universal; Fri, May 26, 1995 11:10 AM

Frame 1	M	S	L	P	A	Q	L	L	G	L	L	L	C	V	P	G	S	S		
	ATG	AGC	CTC	CCT	GCT	CAG	CTC	CTC	GGG	CTG	CTA	TTG	CTC	TGC	GTC	CCC	GGG	TCC	AGT	
			9			18			27			36			45			54		
G	E	V	V	M	T	Q	S	P	L	S	L	P	I	T	P	G	E	P	A	S
GGG	GAA	GTT	GTG	ATG	ACT	CAG	TCT	CCA	CTG	TCC	CTT	CCC	ATC	ACA	CCT	GGA	GAG	CCG	GCC	TCC
	63			72			81			90			99			108			117	
I	S	C	R	S	S	Q	S	L	K	H	S	N	G	D	T	F	L	S	W	Y
ATC	TCC	TGT	AGG	TCT	AGT	CAA	AGC	CTT	AAA	CAC	AGT	AAT	GGA	GAC	ACC	TTC	CTG	AGT	TGG	TAT
	126			135			144			153			162			171			180	
Q	Q	K	P	G	Q	P	P	R	L	L	I	Y	K	V	S	N	R	D	S	G
CAG	CAG	AAG	CCA	GGC	CAA	CCT	CCA	AGG	CTC	CTG	ATT	TAT	AAG	GTT	TCT	AAC	CGG	GAC	TCT	GGG
	189			198			207			216			225			234			243	
V	P	D	R	F	S	G	S	G	A	G	T	D	F	T	L	K	I	S	A	V
GTC	CCA	GAC	AGA	TTC	AGC	GGC	AGT	GGG	GCA	GGG	ACA	GAT	TTC	ACA	CTG	AAA	ATC	AGC	GCA	GTG
	252			261			270			279			288			297			306	
E	A	E	D	V	G	V	Y	F	C	G	Q	G	T	R	T	P	P	T	F	G
GAG	GCT	GAA	GAT	GTT	GGG	GTT	TAT	TTC	TGC	GGG	CAA	GGT	ACA	AGG	ACT	CCT	CCC	ACT	TTC	GGC
	315			324			333			342			351			360			369	
G	G	T	K	V	E	I	K	R	T	V	A	A	P	S	V	F	I	F	P	P
GGA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	CGT	ACG	GTG	GCT	GCA	CCA	TCT	GTC	TTC	ATC	TTC	CCG	CCA
	378			387			396			405			414			423			432	
S	D	E	Q	L	K	S	G	T	A	S	V	V	C	L	L	N	N	F	Y	P
TCT	GAT	GAG	CAG	TTG	AAA	TCT	GGA	ACT	GCC	TCT	GTT	GTG	TGC	CTG	CTG	AAT	AAC	TTC	TAT	CCC
	441			450			459			468			477			486			495	
R	E	A	K	V	Q	W	K	V	D	N	A	L	Q	S	G	N	S	Q	E	S
AGA	GAG	GCC	AAA	GTA	CAG	TGG	AAG	GTG	GAT	AAC	GCC	CTC	CAA	TCG	GGT	AAC	TCC	CAG	GAG	AGT
	504			513			522			531			540			549			558	
V	T	E	Q	D	S	K	D	S	T	Y	S	L	S	S	T	L	T	L	S	K
GTC	ACA	GAG	CAG	GAC	AGC	AAG	GAC	AGC	ACC	TAC	AGC	CTC	AGC	AGC	ACC	CTG	ACG	CTG	AGC	AAA
	567			576			585			594			603			612			621	
A	D	Y	E	K	H	K	V	Y	A	C	E	V	T	H	Q	G	L	S	S	P
GCA	GAC	TAC	GAG	AAA	CAC	AAA	GTC	TAC	GCC	TGC	GAA	GTC	ACC	CAT	CAG	GGC	CTG	AGC	TCG	CCC
	630			639			648			657			666			675			684	
V	T	K	S	F	N	R	G													

FIGURE 4b

Length of 7B6 heavy/Primatized: 1437 bp; Listed from: 1 to: 1437;
 Translated from: 1 to: 1435 (Entire region);
 Genetic Code used: Universal; Fri, May 26, 1995 11:09 AM

Frame 1 M G W S L I L L F L V A V A T R V Q C
 ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT GTC CAG TGT
 9 18 27 36 45 54

E V Q L V E S G G G L V Q P G G S L R V S
 GAG GTG CAA CTG GTG GAG TCT GGG GGA GGC TTG GTC CAG CCT GGC GGG TCC CTG AGA GTC TCC
 63 72 81 90 99 108 117

C A V S G F T F S D H Y M Y W F R Q A P G
 TGT GCA GTC TCT GGA TTC ACC TTC AGT GAC CAC TAC ATG TAT TGG TTC CGC CAG GCT CCA GGG
 126 135 144 153 162 171 180

K G P E W V G F I R N K P N G G T T E Y A
 AAG GGG CCG GAA TGG GTA GGT TTC ATT AGA AAC AAA CCG AAC GGT GGG ACA ACA GAA TAC GCC
 189 198 207 216 225 234 243

A S V K D R F T I S R D D S K S I A Y L Q
 GCG TCT GTG AAA GAC AGA TTC ACC ATC TCC AGA GAT GAT TCC AAA AGC ATC GCC TAT CTG CAA
 252 261 270 279 288 297 306

M S S L K I E D T A V Y Y C T T S Y I S H
 ATG AGC AGC CTG AAA ATC GAG GAC ACG GCC GTC TAT TAC TGT ACT ACA TCC TAC ATT TCA CAT
 315 324 333 342 351 360 369

C R G G V C Y G G Y F E F W G Q G A L V T
 TGT CGG GGT GGT GTC TGC TAT GGA GGT TAC TTC GAA TTC TGG GGC CAG GGC GCC CTG GTC ACC
 378 387 396 405 414 423 432

V S S A S T K G P S V F P L A P S S K S T
 GTC TCC TCA GCT AGC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC
 441 450 459 468 477 486 495

S G G T A A L G C L V K D Y F P E P V T V
 TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG
 504 513 522 531 540 549 558

S W N S G A L T S G V H T F P A V L Q S S
 TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA
 567 576 585 594 603 612 621

G L Y S L S S V V T V P S S S L G T Q T Y
 GGA CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC TAC
 630 639 648 657 666 675 684

I C N V N H K P S N T K V D K K A E P K S
 ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GCA GAG CCC AAA TCT
 693 702 711 720 729 738 747

C D K T H T C P P C P A P E L L G G P S V
 TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC
 756 765 774 783 792 801 810

F L F P P K P K D T L M I S R T P E V T C
 TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC
 819 828 837 846 855 864 873

V V V D V S H E D P E V K F N W Y V D G V
 GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG
 882 891 900 909 918 927 936

FIGURE 4b (Continued)

E	V	H	N	A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V
GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC
945				954			963			972			981			990			999	
S	V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K	V	S
AGC	GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	TCC
1008				1017			1026			1035			1044			1053			1062	
N	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K	G	Q	P	R	E
AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAA
1071				1080			1089			1098			1107			1116			1125	
P	Q	V	Y	T	L	P	P	S	R	D	E	L	T	K	N	Q	V	S	L	T
CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC
1134				1143			1152			1161			1170			1179			1188	
C	L	V	K	G	F	Y	P	S	D	I	A	V	E	W	E	S	N	G	Q	P
TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG
1197				1206			1215			1224			1233			1242			1251	
E	N	N	Y	K	T	T	P	P	V	L	D	S	D	G	S	F	F	L	Y	S
GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC
1260				1269			1278			1287			1296			1305			1314	
K	L	T	V	D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	H
AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT
1323				1332			1341			1350			1359			1368			1377	
E	A	L	H	N	H	Y	T	Q	K	S	L	S	L	S	P	G	K	.		
GAG	GCT	CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA		
1386				1395			1404			1413			1422			1431				

002250-052200

FIGURE

5a

Length of 16C10 Lambda/Primatized : 711 bp;

Listed from: 1 to: 711;

Translated from: 1 to: 709 (Entire region);

Genetic Code used: Universal; Fri, May 26, 1995 11:08 AM

Frame 1 M R V P A Q L L G L L L L W L P G A R
 ATG AGG GTC CCC GCT CAG CTC CTG GGG CTC CTG CTG CTC TGG CTC CCA GGT GCA CGA
 9 18 27 36 45 54

C E S V L T Q P P S V S G A P G Q K V T I
 TGT GAG TCT GTC CTG ACA CAG CCG CCC TCA GTG TCT GGG GCC CCA GGG CAG AAG GTC ACC ATC
 63 72 81 90 99 108 117

S C T G S T S N I G G Y D L H W Y Q Q L P
 TCG TGC ACT GGG AGC ACC TCC AAC ATT GGA GGT TAT GAT CTA CAT TGG TAC CAG CAG CTC CCA
 126 135 144 153 162 171 180

G T A P K L L I Y D I N K R P S G I S D R
 GGA ACG GCC CCC AAA CTC CTC ATC TAT GAC ATT AAC AAG CGA CCC TCA GGA ATT TCT GAC CGA
 189 198 207 216 225 234 243

F S G S K S G T A A S L A I T G L Q T E D
 TTG TCT GGC TCC AAG TCT GGT ACC GCG GCC TCC CTG GCC ATC ACT GGG CTC CAG ACT GAG GAT
 252 261 270 279 288 297 306

E A D Y Y C Q S Y D S S L N A Q V F G G G
 GAG GCT GAT TAT TAC TGC CAG TCC TAT GAC AGC AGC CTG AAT GCT CAG GTA TTC GGA GGA GGG
 315 324 333 342 351 360 369

T R L T V L G Q P K A A P S V T L F P P S
 ACC CGG CTG ACC GTC CTA GGT CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC TCC
 378 387 396 405 414 423 432

S E E L Q A N K A T L V C L I S D F Y P G
 TCT GAG GAG CTT CAA GCC AAC AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC TTC TAC CCG GGA
 441 450 459 468 477 486 495

A V T V A W K A D S S P V K A G V E T T T
 GCC GTG ACA GTG GCC TGG AAG GCA GAT AGC AGC CCC GTC AAG GCG GGA GTG GAG ACC ACC ACA
 504 513 522 531 540 549 558

P S K Q S N N K Y A A S S Y L S L T P E Q
 CCC TCC AAA CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG
 567 576 585 594 603 612 621

W K S H R S Y S C Q V T H E G S T V E K T
 TGG AAG TCC CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG GAG AAG ACA
 630 639 648 657 666 675 684

V A P T E C S
 GTG GCC CCT ACA GAA TGT TCA TGA
 693 702 711

FIGURE 5b

Length of 16C10 heavy/primatized: 1431 bp;
 Listed from: 1 to: 1431;
 Translated from: 1 to: 1429 (Entire region);
 Genetic Code used: Universal; Fri, May 26, 1995 11:08 AM

Frame 1 M K H L W F F L L L V A A P R W V L S
 ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA TGG GTC CTG TCC
 9 18 27 36 45 54

Q V Q L Q E S G P G L V K P S E T L S L T
 CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC
 63 72 81 90 99 108 117

C A V S G G S I S G G Y G W G W I R Q P P
 TGC GCT GTC TCT GGT GGC TCC ATC AGC GGT GGT TAT GGC TGG GGC TGG ATC CGC CAG CCC CCA
 126 135 144 153 162 171 180

G K G L E W I G S F Y S S S G N T Y Y N P
 GGG AAG GGG CTG GAG TGG ATT GGG AGT TTC TAT AGT AGT AGT GGG AAC ACC TAC TAC AAC CCC
 189 198 207 216 225 234 243

S L K S Q V T I S T D T S K N Q F S L K L
 TCG CTC AAG AGT CAA GTC ACC ATT TCA ACA GAC ACG TCC AAG AAC CAG TTC TCC CTG AAG CTG
 252 261 270 279 288 297 306

N S M T A A D T A V Y Y C V R D R L F S V
 AAC TCT ATG ACC GCC GCG GAC ACG GCC GTG TAT TAC TGT GTG AGA GAT CGT CTT TTT TCA GTT
 315 324 333 342 351 360 369

V G M V Y N N W E D V W G P G V L V T V S
 GGA ATG GTT TAC AAC AAC TGG TTC GAT GTC TGG GGC CCG GGA GTC CTG GTC ACC GTC TCC
 378 387 396 405 414 423 432

S A S T K G P S V F P L A P S S K S T S G
 TCA GCT AGC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG
 441 450 459 468 477 486 495

G T A A L G C L V K D Y F P E P V T V S W
 GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG
 504 513 522 531 540 549 558

N S G A L T S G V H T F P A V L Q S S G L
 AAC TCA GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC
 567 576 585 594 603 612 621

Y S L S S V V T V P S S S L G T Q T Y I C
 TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC TAC ATC TGC
 630 639 648 657 666 675 684

N V N H K P S N T K V D K K A E P K S C D
 AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GCA GAG CCC AAA TCT TGT GAC
 693 702 711 720 729 738 747

K T H T C P P C P A P E L L G G P S V F L
 AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC
 756 765 774 783 792 801 810

F P P K P K D T L M I S R T P E V T C V V
 TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG
 819 828 837 846 855 864 873

V D V S H E D P E V K F N W Y V D G V E V
 GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG

FIGURE 5b (Continued)

882	891	900	909	918	927	936
H N A K T K P R E E Q Y N S T Y R V V S V						
CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC						
945	954	963	972	981	990	999
L T V L H Q D W L N G K E Y K C K V S N K						
CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA						
1008	1017	1026	1035	1044	1053	1062
A L P A P I E K T I S K A K G Q P R E P Q						
GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG						
1071	1080	1089	1098	1107	1116	1125
V Y T L P P S R D E L T K N Q V S L T C L						
GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG						
1134	1143	1152	1161	1170	1179	1188
V K G F Y P S D I A V E W E S N G Q P E N						
GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC						
1197	1206	1215	1224	1233	1242	1251
N Y K T T P P V L D S D G S F F L Y S K L						
AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC						
1260	1269	1278	1287	1296	1305	1314
T V D K S R W Q Q G N V F S C S V M H E A						
ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT						
1323	1332	1341	1350	1359	1368	1377
L H N H Y T Q K S L S L S P G K						
CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA						
1386	1395	1404	1413	1422	1431	

002256-149460

Figure 6

Competitive Binding of CTLA-4Ig-Biotin to B7-1 Transfected CHO Cells
in Presence of P16C10 MA b, CTLA-4Ig and B7-1Ig Fusion Proteins

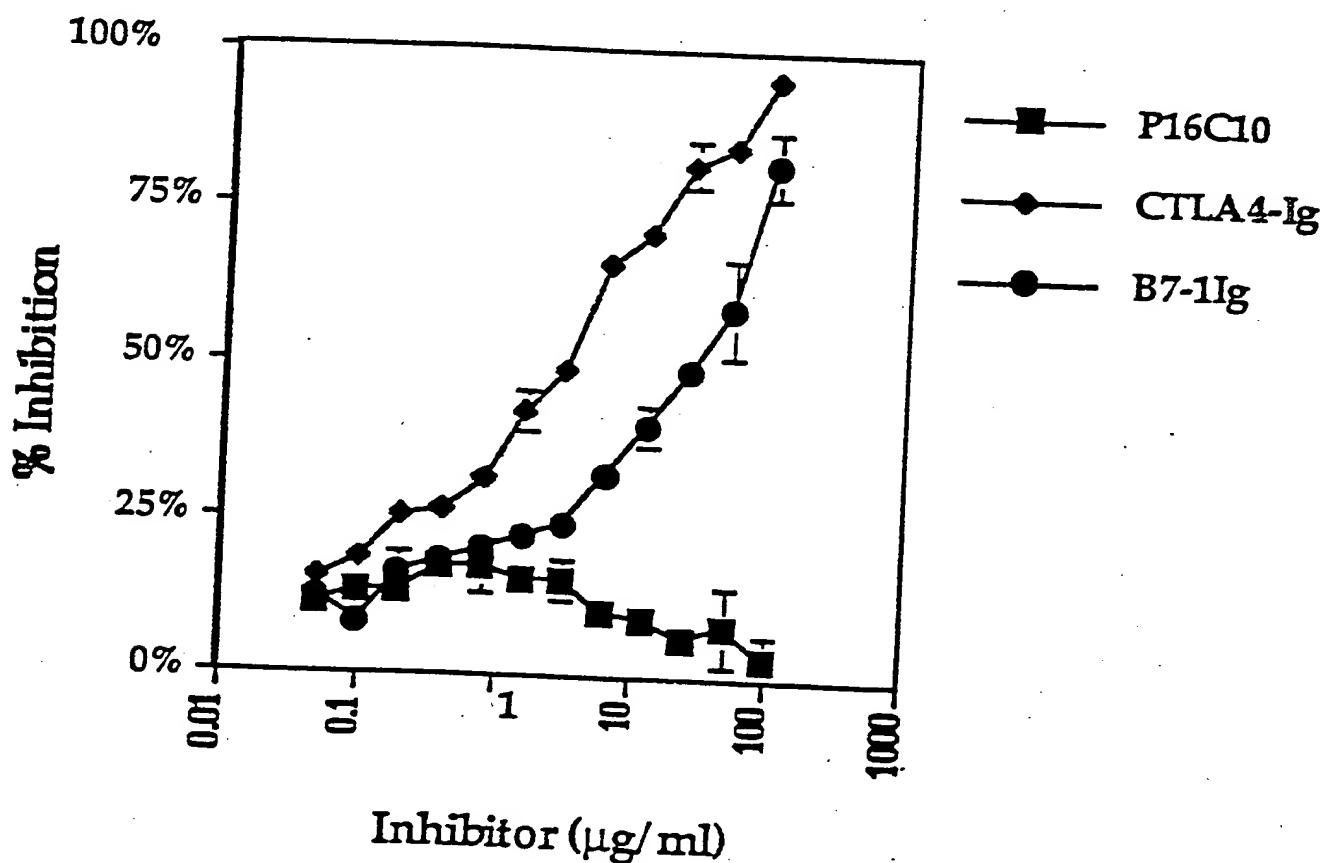


Figure 7

Competitive Binding of P16C10-Biotin to B7-1 Transfected CHO Cells
in Presence of P16C10 MAb, CTLA-4Ig and B7-1Ig Fusion Proteins

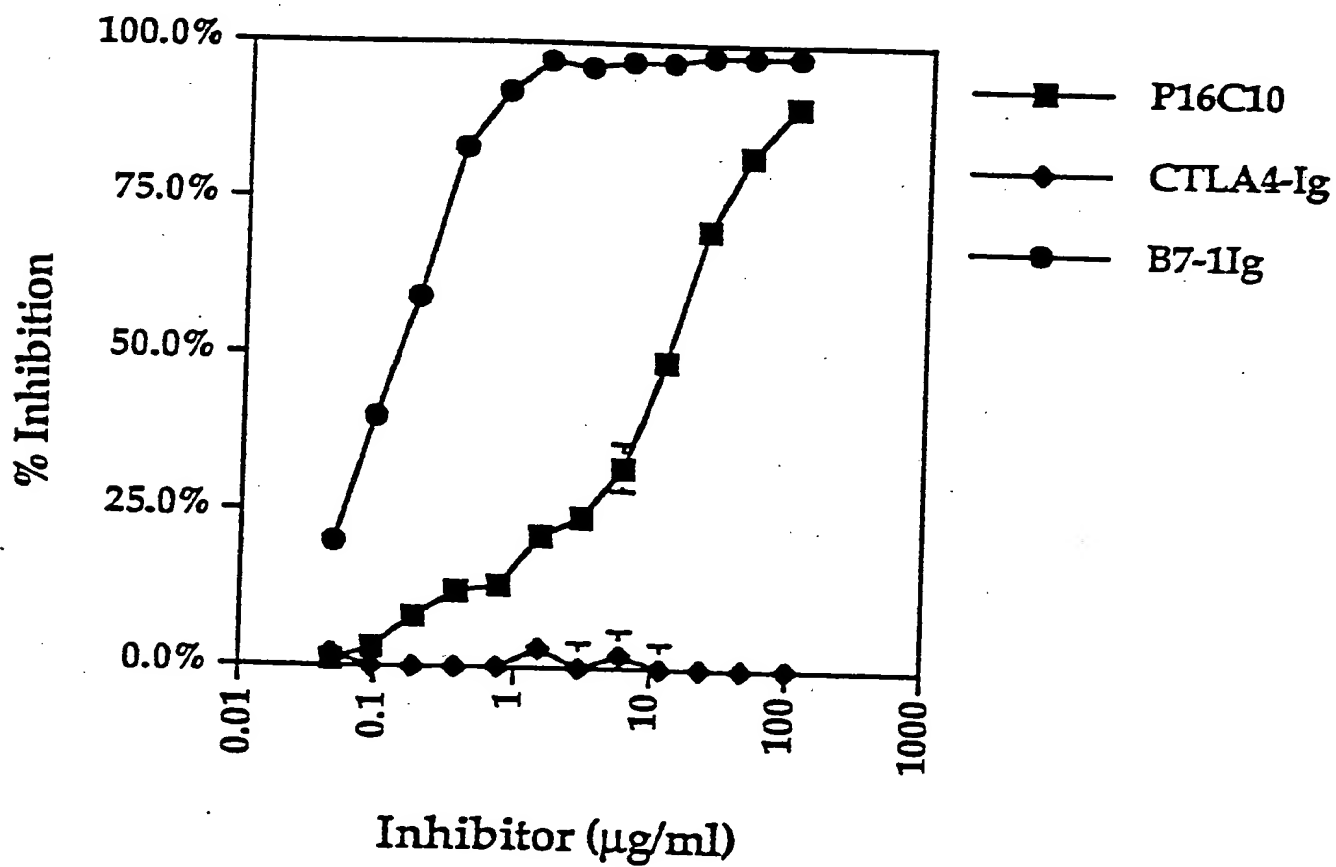


Figure 8

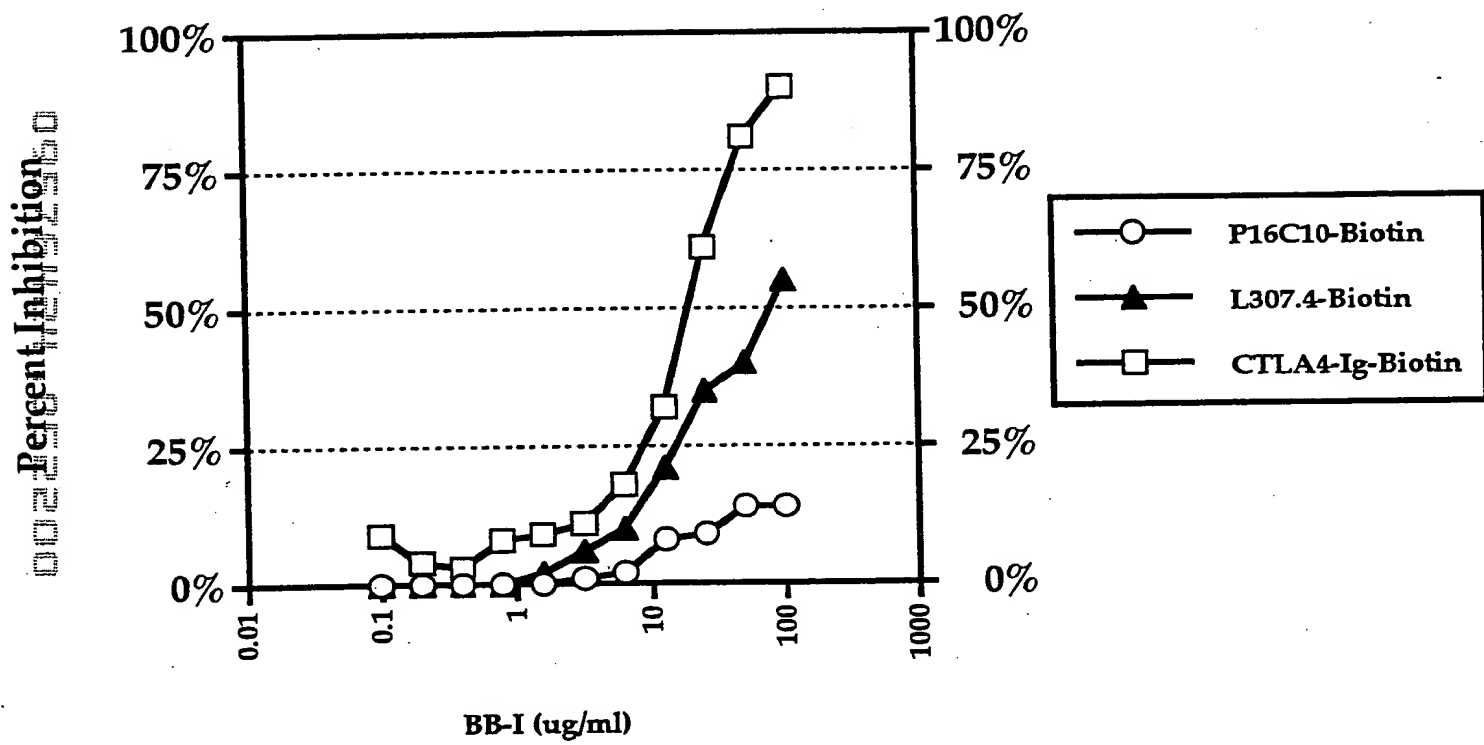
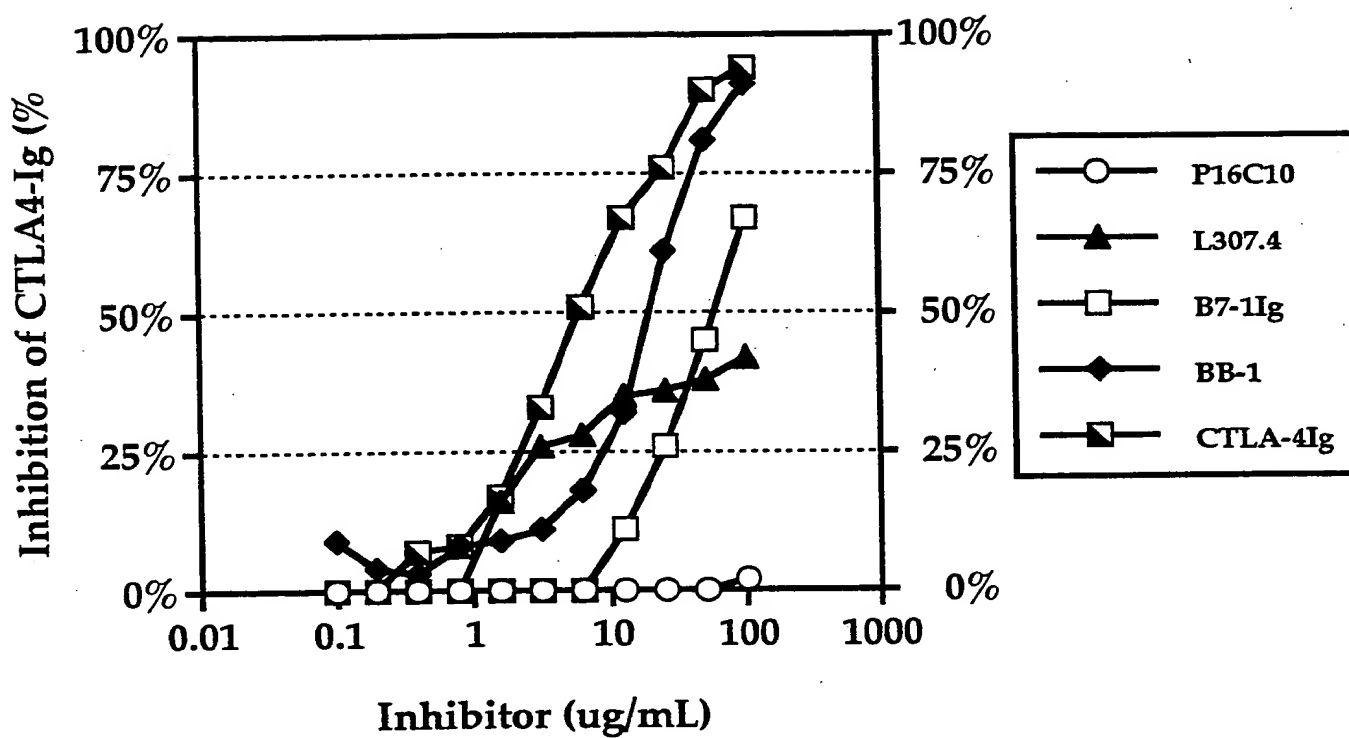


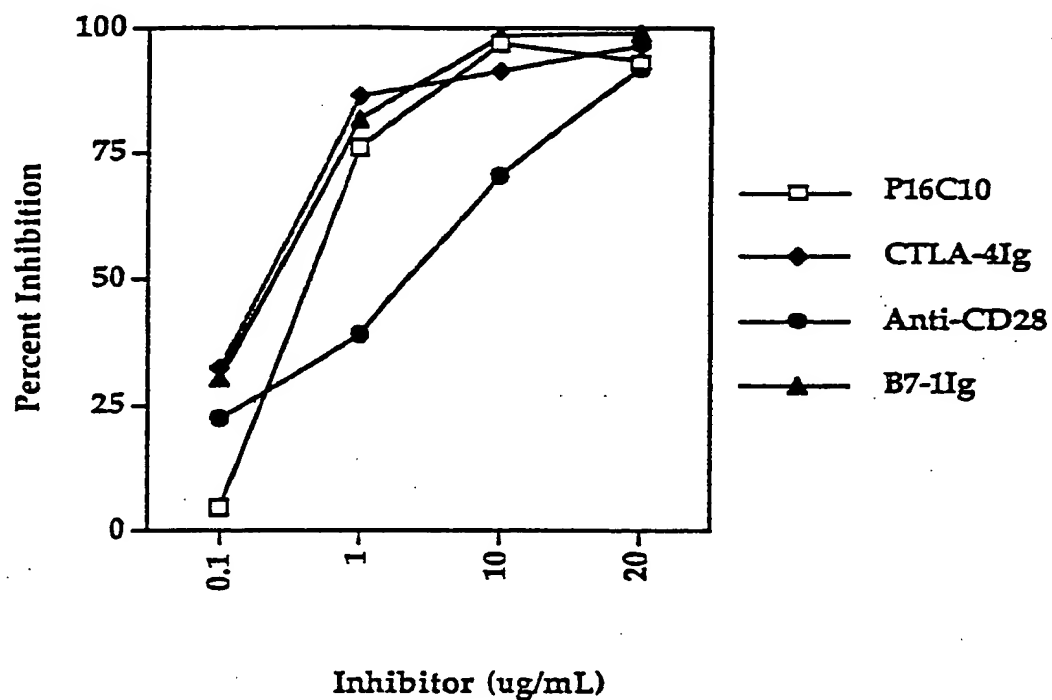
Figure 9



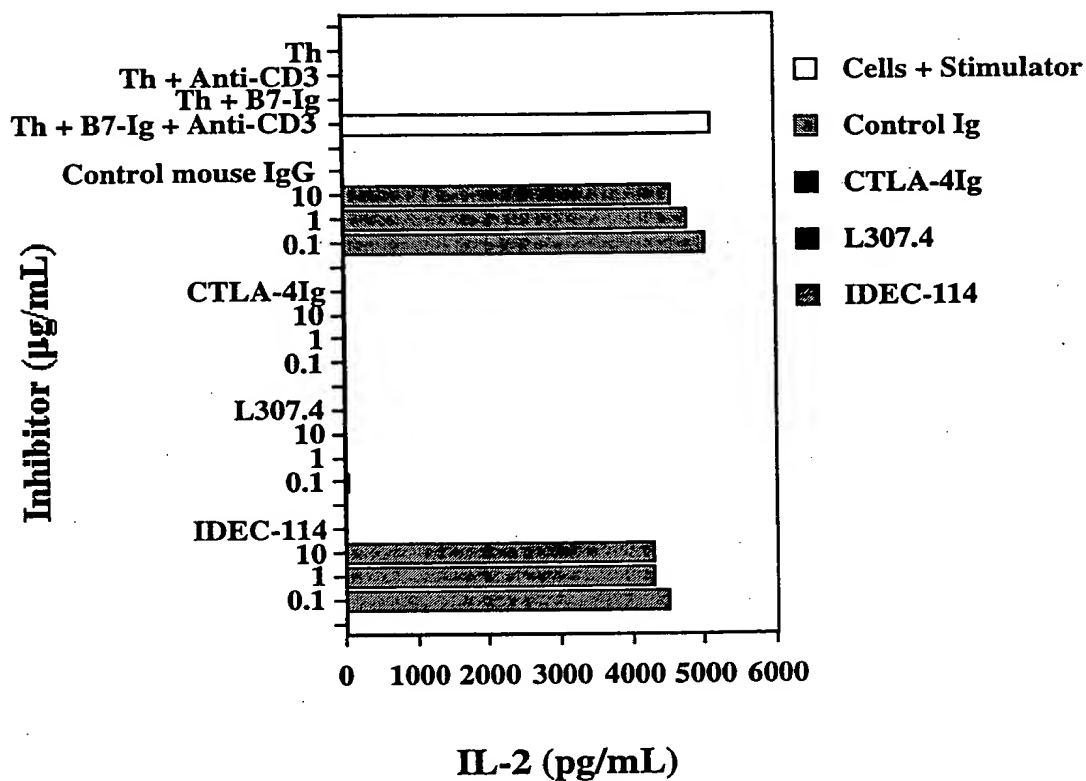
002250-172494560

Figure 10

Competitive Inhibition of Radiolabeled B7-1Ig Binding to CD28 Receptors on Isolated Non-Activated Peripheral Blood T Cells using Unlabeled Binding Proteins Recognizing Either B7-1 or CD28



IDEC-114 Does Not Block IL-2 Production Induced by Co-stimulation with Anti-CD3 and B7Ig Coated Latex Microspheres



Figure/1: Production of IL-2 in cultures of purified normal human CD4+ lymphocytes when stimulated with sub-optimal amounts of immobilized anti-CD3 antibody and B7-1 (CD80) on latex microbeads. L307.4 is a commercially available murine antibody (B/D Pharmingen) that binds specifically to human CD80 and neutralizes CD28:CD80 functional interactions. CTLA-4Ig is a soluble receptor fusion protein that specifically blocks CD80 and CD86 binding to CD28 receptors on T cells. IDEC-114 is a PRIMATIZED monoclonal antibody that specifically binds to both soluble and membrane forms of the CD80 antigen but does not recognize CTLA-4 or B7-2 antigens. The ratio of anti-CD3 to B7Ig used in the cultures to stimulate T cells was 1:10 (w/w).

IDEC-114 Does Not Block T cell Growth When Co-stimulated by Anti-CD3 and B7Ig Coated Latex Microspheres

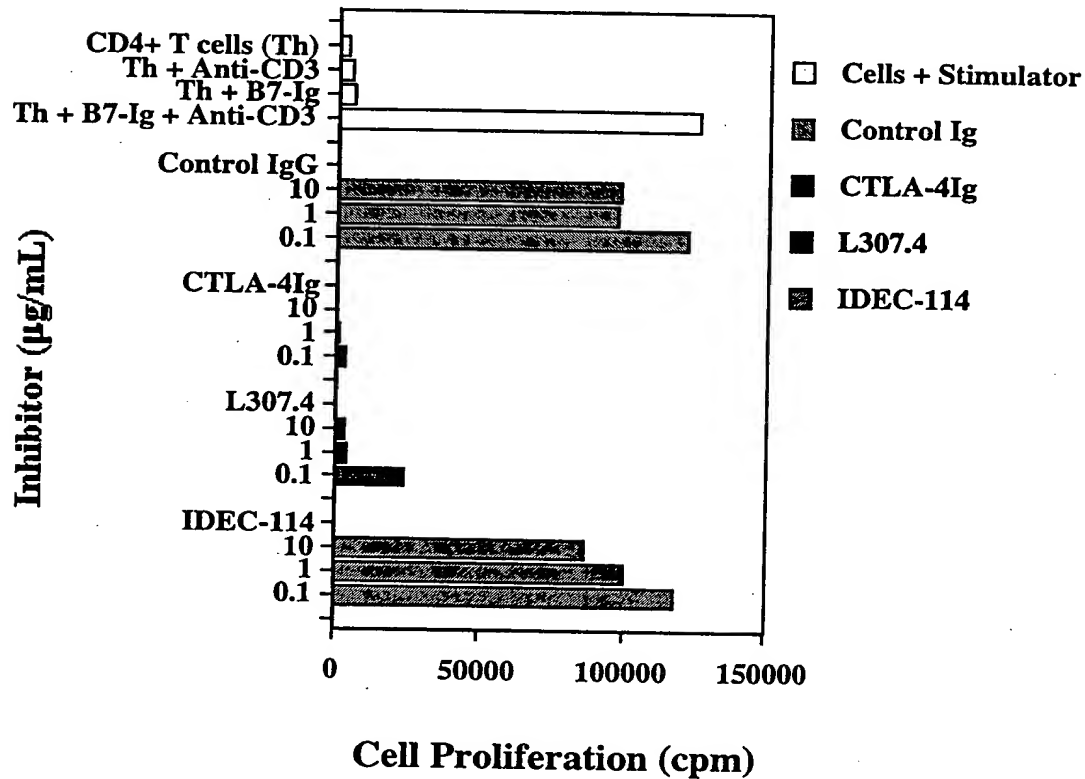


Figure 2: Uptake of H3-Thymidine in cultures of purified normal human CD4+ lymphocytes when stimulated with sub-optimal amounts of immobilized anti-CD3 antibody and B7-1 (CD80) on latex microbeads. L307.4 is a commercially available murine antibody (B/D Pharmingen) that binds specifically to human CD80 and neutralizes CD28:CD80 functional interactions. CTLA-4Ig is a soluble receptor fusion protein that specifically blocks CD80 and CD86 binding to CD28 receptors on T cells. IDEC-114 is a PRIMATIZED monoclonal antibody that specifically binds to both soluble and membrane forms of the CD80 antigen but does not recognize CTLA-4 or B7-2 antigens.

Production of IL-10 by Co-stimulation with Anti-CD3:B7-Ig (1:10) Latex Microspheres is Inhibited by CTLA-4Ig, and Anti-CD80 Antibodies L307.4 and IDEC-114

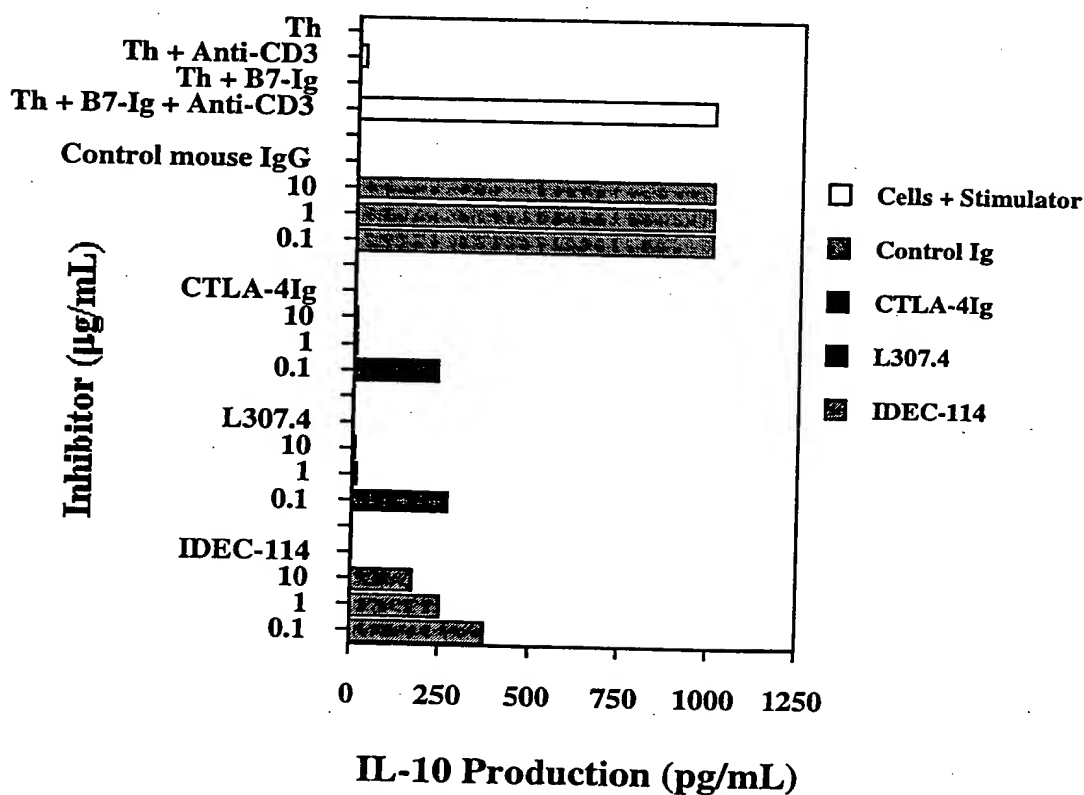


Figure 3: Production of TH2 cytokine IL-10 in cultures of purified normal human CD4+ lymphocytes when stimulated with sub-optimal amounts of immobilized anti-CD3 antibody and B7-1 (CD80) on latex microbeads. Inhibition of IL-10 production by L307.4 anti-CD80 and CTLA-4Ig fusion protein was compared at 0.1, 1, and 10 µg/mL.

IDEC-114 Blocks IL-2 Production by Purified CD4+ T Cells When Low Bead Densities of B7 are Used as Stimulators

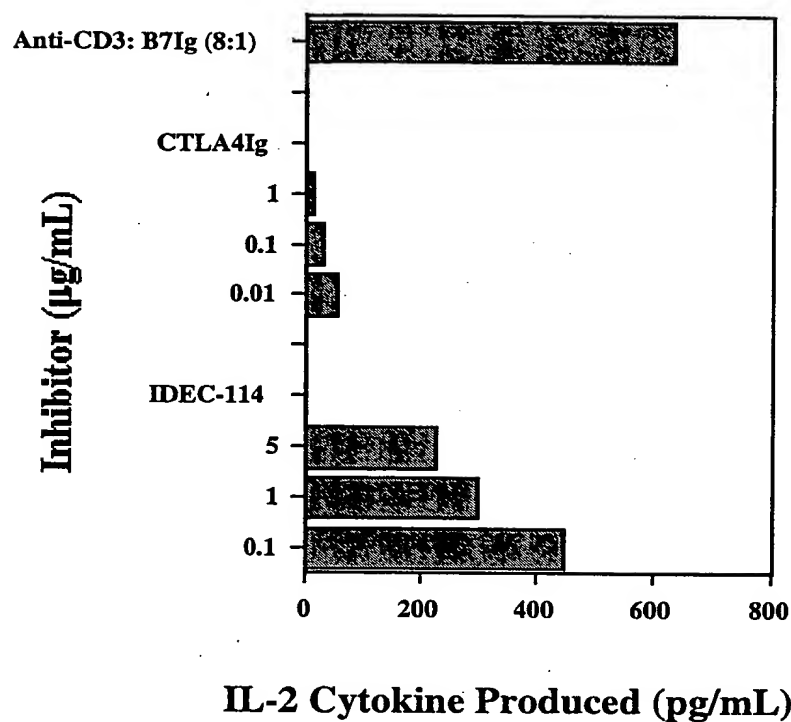


Figure4: Inhibition of IL-2 cytokine production by CTLA-4Ig and IDEC-114 in cultures of purified human CD4+ T cells. T cells were co-stimulated with anti-CD3 and B7Ig coated latex microbeads with an anti-CD3/B7 ratio (w/w) of 8:1. IL-2 was determined by growth and uptake of Thymidine by the IL-2 dependent cell line CTLL-2.